

## SEQUENCE LISTING

&lt;110&gt; Degussa AG

5 &lt;120&gt; Feedback Resistant Mutants

&lt;130&gt; 020191 AM

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 12

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

20

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: modified AHAS

&lt;220&gt;

25 &lt;221&gt; CDS

&lt;222&gt; (1) .. (519)

&lt;400&gt; 1

atg gct aat tct gac gtc acc ogc cac atc ctg tcc gta ctc gtt cag 48

30 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln

1

5

10

15

gac gta gac gat gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc 96  
 Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg  
 20 25 30

5 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc 144  
 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly  
 35 40 45

atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag 192  
 10 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu  
 50 55 60

cag atc acc aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg 240  
 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val  
 15 65 70 75 80

cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag 288  
 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys  
 85 90 95

20 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac 336  
 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn  
 100 105 110

25 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att 384  
 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile  
 115 120 125

gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg 432  
 30 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met  
 130 135 140

gaa cca ttc gga atc cgc gaa ctg atc caa tcc gga cag att gca ctc 480  
 Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu  
 145 150 155 160

5 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa 519  
 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile  
 165 170

10 <210> 2  
 <211> 173  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: modified AHAS

15  
 <400> 2  
 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln  
 1 5 10 15  
 20 Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg  
 20 25 30  
 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly  
 35 40 45  
 25 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu  
 50 55 60  
 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val  
 30 65 70 75 80  
 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys  
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn  
 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile  
 5 115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met  
 130 135 140

10 Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu  
 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile  
 165 170  
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<210> 3

<211> 519

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: modified AHAS

25 <220>

<221> CDS

<222> (1)..(519)

<400> 3

30 atg gct aat tct gac gtc acc cgc cac atc ctg tcc gta ctc gtt cag 48

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln

1

5

10

15

gac gta gac ggt gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc 96  
 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg

20

25

30

5 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc 144  
 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly

35

40

45

atc aac cgc atc acg gtt gtt gtc gac gcc gac gag ctc aac att gag 192  
 10 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu

50

55

60

cag atc acc aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg 240  
 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val

15

65

70

75

80

cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag 288  
 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys

85

90

95

20

gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac 336  
 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn

100

105

110

25 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att 384  
 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile

115

120

125

gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg 432  
 30 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met

130

135

140

gaa cca ttc gga atc cgc gaa ctg atc caa tcc gga cag att gca ctc 480  
 Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu  
 145 150 155 160

5 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa 519  
 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile  
 165 170

10 <210> 4  
 <211> 173  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: modified AHAS

15  
 <400> 4  
 Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln  
 1 5 10 15

20 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg  
 20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly  
 35 40 45

25 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu  
 50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val  
 30 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys  
 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn

100

105

110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile

5

115

120

125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met

130

135

140

10

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu

145

150

155

160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile

15

165

170

&lt;210&gt; 5

&lt;211&gt; 17

20 &lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Primer

25

&lt;400&gt; 5

gcggaggaag tactgcc

17

30 &lt;210&gt; 6

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 6

5 caatcagatt aattgctggt ta

22

<210> 7

<211> 26

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

15

<400> 7

ggacgtagac ggtgacatgt cccgcg

26

20 <210> 8

<211> 19

<212> DNA

<213> Artificial Sequence

25 <220>

<223> Description of Artificial Sequence:Primer

<400> 8

gtttagaact tggccggag

19

30

<210> 9

<211> 20

<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

5

<400> 9

gatcctgccg acattcacga

20

10 <210> 10

<211> 57

<212> PRT

<213> *Corynebacterium glutamicum*

15 <400> 10

Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln

1

5

10

15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg

20

20

25

30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly

35

40

45

25 Ile Asn Arg Ile Thr Val Val Val Asp

50

55

<210> 11

30 <211> 53

<212> PRT

<213> *S. cinnamomensis*

<400> 11

10

Met Ser Thr Lys His Thr Leu Ser Val Leu Val Glu Asn Lys Pro Gly

1 5 10 15

Val Leu Ala Arg Ile Thr Ala Leu Phe Ser Arg Arg Gly Phe Asn Ile

5 20 25 30

Asp Ser Leu Ala Val Gly Val Thr Glu His Pro Asp Ile Ser Arg Ile

35 40 45

10 Thr Ile Val Val Asn

50

&lt;210&gt; 12

15 &lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Escherichia Coli

&lt;400&gt; 12

20 Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg

1 5 10 15

Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg

20 25 30

25

Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp

35 40 45

Lys Ser His Ile Trp Leu Leu Val Asn

30 50 55